

STIC Biotechnology Systems Branch

RAW SEQUENCE LISTING

ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/572,189
Source: IFWP
Date Processed by STIC: 04/06/2006

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.4.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , **EFS Submission User Manual - ePAVE**)
2. **U.S. Postal Service:** Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. **Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05):**
U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/10/06

Raw Sequence Listing Error Summary

<u>ERROR DETECTED</u>	<u>SUGGESTED CORRECTION</u>	SERIAL NUMBER: <u>10/572,189</u>
ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE		
1 _____ Wrapped Nucleics Wrapped Aminos	The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."	
2 _____ Invalid Line Length	The rules require that a line not exceed 72 characters in length. This includes white spaces.	
3 _____ Misaligned Amino Numbering	The numbering under each 5 th amino acid is misaligned. Do not use tab codes between numbers; use space characters , instead.	
4 _____ Non-ASCII	The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.	
5 _____ Variable Length	Sequence(s) _____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.	
6 _____ PatentIn 2.0 "bug"	A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.	
7 _____ Skipped Sequences (OLD RULES)	Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence: (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading) (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) This sequence is intentionally skipped Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.	
8 _____ Skipped Sequences (NEW RULES)	Sequence(s) _____ missing. If intentional , please insert the following lines for each skipped sequence. <210> sequence id number <400> sequence id number 000	
9 _____ Use of n's or Xaa's (NEW RULES)	Use of n's and/or Xaa's have been detected in the Sequence Listing. Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa , and which residue n or Xaa represents.	
10 _____ Invalid <213> Response	Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence. (see item 11 below)	
11 _____ Use of <220>	Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section or use "chemically synthesized" as explanation. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32), also Sec. 1.823 of Sequence Rules	
12 _____ PatentIn 2.0 "bug"	Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.	
13 _____ Misuse of n/Xaa	"n" can only represent a single nucleotide; "Xaa" can only represent a single amino acid	



IFWP

RAW SEQUENCE LISTING

DATE: 04/06/2006

PATENT APPLICATION: US/10/572,189

TIME: 10:45:48

Input Set : A:\Sequence Listing (13111-00033-US).txt

Output Set: N:\CRF4\04062006\J572189.raw

3 <110> APPLICANT: Ostermann, Kai
 4 Rodel, Gerhard
 6 <120> TITLE OF INVENTION: SECRETION OF PROTEINS FROM YEASTS
 8 <130> FILE REFERENCE: 13111-00033-US
 C--> 10 <140> CURRENT APPLICATION NUMBER: US/10/572,189
 C--> 10 <141> CURRENT FILING DATE: 2006-03-15
 10 <150> PRIOR APPLICATION NUMBER: PCT/EP2004/010346
 11 <151> PRIOR FILING DATE: 2004-09-15
 13 <150> PRIOR APPLICATION NUMBER: DE 103 42 794.5
 14 <151> PRIOR FILING DATE: 2003-09-16
 16 <160> NUMBER OF SEQ ID NOS: 56
 18 <170> SOFTWARE: PatentIn version 3.3
 20 <210> SEQ ID NO: 1
 22 <211> LENGTH: 171
 24 <212> TYPE: DNA
 26 <213> ORGANISM: Schizosaccharomyces pombe
 29 <220> FEATURE:
 31 <221> NAME/KEY: CDS
 33 <222> LOCATION: (1)..(171)
 35 <400> SEQUENCE: 1
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 37 Met Lys Ile Thr Ala Val Ile Ala Leu Leu Phe Ser Leu Ala Ala Ala
 38 1 5 10 15
 40 tca cct att cca gtt gcc gat cct ggt gtg gtt tca gtt agc aag tca 96
 41 Ser Pro Ile Pro Val Ala Asp Pro Gly Val Val Ser Val Ser Lys Ser
 42 20 25 30
 44 tat gct gat ttc ctt cgt gtt tac caa agt tgg aac act ttt gct aat 144
 45 Tyr Ala Asp Phe Leu Arg Val Tyr Gln Ser Trp Asn Thr Phe Ala Asn
 46 35 40 45
 48 cct gat aga ccc aac ttg aaa aag cgc 171
 49 Pro Asp Arg Pro Asn Leu Lys Lys Arg
 50 50 55
 53 <210> SEQ ID NO: 2
 55 <211> LENGTH: 57
 57 <212> TYPE: PRT
 59 <213> ORGANISM: Schizosaccharomyces pombe
 62 <400> SEQUENCE: 2
 64 Met Lys Ile Thr Ala Val Ile Ala Leu Leu Phe Ser Leu Ala Ala Ala
 65 1 5 10 15
 68 Ser Pro Ile Pro Val Ala Asp Pro Gly Val Val Ser Val Ser Lys Ser
 69 20 25 30
 72 Tyr Ala Asp Phe Leu Arg Val Tyr Gln Ser Trp Asn Thr Phe Ala Asn
 73 35 40 45

Does Not Comply
 Corrected Diskette Needed

(Pg-5)

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82 <211> LENGTH: 60
84 <212> TYPE: DNA
86 <213> ORGANISM: Schizosaccharomyces pombe
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92 <221> NAME/KEY: CDS
94 <222> LOCATION: (1)..(60)
97 <220> FEATURE:
99 <221> NAME/KEY: sig_peptide
101 <222> LOCATION: (1)..(60)
105 <400> SEQUENCE: 3
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108 1                      5                      10                      15
110 tca cct att cca                                          60
111 Ser Pro Ile Pro
112      20
115 <210> SEQ ID NO: 4
117 <211> LENGTH: 20
119 <212> TYPE: PRT
121 <213> ORGANISM: Schizosaccharomyces pombe
124 <400> SEQUENCE: 4
126 Met Lys Ile Thr Ala Val Ile Ala Leu Leu Phe Ser Leu Ala Ala Ala
127 1                      5                      10                      15
130 Ser Pro Ile Pro
131      20
134 <210> SEQ ID NO: 5
136 <211> LENGTH: 81
138 <212> TYPE: DNA
140 <213> ORGANISM: Schizosaccharomyces pombe
143 <220> FEATURE:
145 <221> NAME/KEY: CDS
147 <222> LOCATION: (1)..(81)
150 <400> SEQUENCE: 5
151 aag tca tat gct gat ttc ctt cgt gtt tac caa agt tgg aac act ttt      48
152 Lys Ser Tyr Ala Asp Phe Leu Arg Val Tyr Gln Ser Trp Asn Thr Phe
153 1                      5                      10                      15
155 gct aat cct gat aga ccc aac ttg aaa aag cgc                                          81
156 Ala Asn Pro Asp Arg Pro Asn Leu Lys Lys Arg
157      20                      25
160 <210> SEQ ID NO: 6
162 <211> LENGTH: 27
164 <212> TYPE: PRT
166 <213> ORGANISM: Schizosaccharomyces pombe
170 <400> SEQUENCE: 6
172 Lys Ser Tyr Ala Asp Phe Leu Arg Val Tyr Gln Ser Trp Asn Thr Phe
173 1                      5                      10                      15

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Input Set : A:\Sequence Listing (13111-00033-US).txt

Output Set: N:\CRF4\04062006\J572189.raw

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176 Ala Asn Pro Asp Arg Pro Asn Leu Lys Lys Arg
177          20          25
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182 <211> LENGTH: 78
184 <212> TYPE: DNA
186 <213> ORGANISM: Schizosaccharomyces pombe
190 <220> FEATURE:
192 <221> NAME/KEY: CDS
194 <222> LOCATION: (1)..(78)
198 <220> FEATURE:
200 <221> NAME/KEY: sig_peptide
202 <222> LOCATION: (1)..(60)
206 <400> SEQUENCE: 7
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209 1          5          10          15
211 tca cct att cca gtt gcc gat cct ggt gtg      78
212 Ser Pro Ile Pro Val Ala Asp Pro Gly Val
213          20          25
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218 <211> LENGTH: 26
220 <212> TYPE: PRT
222 <213> ORGANISM: Schizosaccharomyces pombe
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229 1          5          10          15
232 Ser Pro Ile Pro Val Ala Asp Pro Gly Val
233          20          25
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238 <211> LENGTH: 606
240 <212> TYPE: DNA
242 <213> ORGANISM: Schizosaccharomyces pombe
246 <220> FEATURE:
248 <221> NAME/KEY: CDS
250 <222> LOCATION: (1)..(606)
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257 1          5          10          15
259 tca cct att cca gtt gcc gat cct ggt gtg gtt tca gtt agc aag tca      96
260 Ser Pro Ile Pro Val Ala Asp Pro Gly Val Val Ser Val Ser Lys Ser
261          20          25          30
263 tat gct gat ttc ctt cgt gtt tac caa agt tgg aac act ttt gct aat      144
264 Tyr Ala Asp Phe Leu Arg Val Tyr Gln Ser Trp Asn Thr Phe Ala Asn
265          35          40          45
267 cct gat aga ccc aac ttg aaa aag cgc gaa ttc gaa gct gct ccc gca      192
268 Pro Asp Arg Pro Asn Leu Lys Lys Arg Glu Phe Glu Ala Ala Pro Ala
269          50          55          60
271 aaa act tat gct gat ttc ctt cgt gct tat caa agt tgg aac act ttt      240

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272 Lys Thr Tyr Ala Asp Phe Leu Arg Ala Tyr Gln Ser Trp Asn Thr Phe
273 65          70          75          80
275 gtt aat cct gac aga ccc aat ttg aaa aag cgt gag ttt gaa gct gcc      288
276 Val Asn Pro Asp Arg Pro Asn Leu Lys Lys Arg Glu Phe Glu Ala Ala
277          85          90          95
279 cca gag aag agt tat gct gat ttc ctt cgt gct tac cat agt tgg aac      336
280 Pro Glu Lys Ser Tyr Ala Asp Phe Leu Arg Ala Tyr His Ser Trp Asn
281          100          105          110
283 act ttt gtt aat cct gac aga ccc aac ttg aaa aag cgc gaa ttc gaa      384
284 Thr Phe Val Asn Pro Asp Arg Pro Asn Leu Lys Lys Arg Glu Phe Glu
285          115          120          125
287 gct gct ccc gca aaa act tat gct gat ttc ctt cgt gct tac caa agt      432
288 Ala Ala Pro Ala Lys Thr Tyr Ala Asp Phe Leu Arg Ala Tyr Gln Ser
289          130          135          140
291 tgg aac act ttt gtt aat cct gac aga ccc aac ttg aaa aag cgc act      480
292 Trp Asn Thr Phe Val Asn Pro Asp Arg Pro Asn Leu Lys Lys Arg Thr
293 145          150          155          160
295 gaa gaa gat gaa gag aat gag gaa gag gat gaa gaa tac tat cgc ttt      528
296 Glu Glu Asp Glu Glu Asn Glu Glu Glu Asp Glu Glu Tyr Tyr Arg Phe
297          165          170          175
299 ctt cag ttt tat atc atg act gtc cca gag aat tcc act att aca gat      576
300 Leu Gln Phe Tyr Ile Met Thr Val Pro Glu Asn Ser Thr Ile Thr Asp
301          180          185          190
303 gtc aat att act gcc aaa ttt gag agc taa      606
304 Val Asn Ile Thr Ala Lys Phe Glu Ser
305          195          200
308 <210> SEQ ID NO: 10
310 <211> LENGTH: 201
312 <212> TYPE: PRT
314 <213> ORGANISM: Schizosaccharomyces pombe
318 <400> SEQUENCE: 10
320 Met Lys Ile Thr Ala Val Ile Ala Leu Leu Phe Ser Leu Ala Ala Ala
321 1          5          10          15
324 Ser Pro Ile Pro Val Ala Asp Pro Gly Val Val Ser Val Ser Lys Ser
325          20          25          30
328 Tyr Ala Asp Phe Leu Arg Val Tyr Gln Ser Trp Asn Thr Phe Ala Asn
329          35          40          45
332 Pro Asp Arg Pro Asn Leu Lys Lys Arg Glu Phe Glu Ala Ala Pro Ala
333          50          55          60
336 Lys Thr Tyr Ala Asp Phe Leu Arg Ala Tyr Gln Ser Trp Asn Thr Phe
337 65          70          75          80
340 Val Asn Pro Asp Arg Pro Asn Leu Lys Lys Arg Glu Phe Glu Ala Ala
341          85          90          95
344 Pro Glu Lys Ser Tyr Ala Asp Phe Leu Arg Ala Tyr His Ser Trp Asn
345          100          105          110
348 Thr Phe Val Asn Pro Asp Arg Pro Asn Leu Lys Lys Arg Glu Phe Glu
349          115          120          125
352 Ala Ala Pro Ala Lys Thr Tyr Ala Asp Phe Leu Arg Ala Tyr Gln Ser
353          130          135          140

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356 Trp Asn Thr Phe Val Asn Pro Asp Arg Pro Asn Leu Lys Lys Arg Thr
 357 145 150 155 160
 360 Glu Glu Asp Glu Glu Asn Glu Glu Glu Asp Glu Glu Tyr Tyr Arg Phe
 361 165 170 175
 364 Leu Gln Phe Tyr Ile Met Thr Val Pro Glu Asn Ser Thr Ile Thr Asp
 365 180 185 190
 368 Val Asn Ile Thr Ala Lys Phe Glu Ser
 369 195 200
 372 <210> SEQ ID NO: 11
 374 <211> LENGTH: 156
 376 <212> TYPE: DNA
 378 <213> ORGANISM: Unknown
 382 <220> FEATURE:
 384 <223> OTHER INFORMATION: to be completed
 387 <220> FEATURE:
 389 <221> NAME/KEY: CDS
 391 <222> LOCATION: (1)..(156)
 395 <400> SEQUENCE: 11
 396 ctg gtt ccg cgt gga tcc atc gaa ggt cgt ggc ggc cgc atc ttt tac 48
 397 Leu Val Pro Arg Gly Ser Ile Glu Gly Arg Gly Gly Arg Ile Phe Tyr
 398 1 5 10 15
 400 cca tac gat gtt cct gac tat gcg ggc tat ccc tat gac gtc ccg gac 96
 401 Pro Tyr Asp Val Pro Asp Tyr Ala Gly Tyr Pro Tyr Asp Val Pro Asp
 402 20 25 30
 404 tat gca gga tcc tat cca tat gac gtt cca gat tac gct gct cag tgc 144
 405 Tyr Ala Gly Ser Tyr Pro Tyr Asp Val Pro Asp Tyr Ala Ala Gln Cys
 406 35 40 45
 408 ggc cgc taa tag 156
 409 Gly Arg
 410 50
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 415 <211> LENGTH: 50
 417 <212> TYPE: PRT
 419 <213> ORGANISM: Unknown
 423 <220> FEATURE:
 425 <223> OTHER INFORMATION: to be completed
 428 <400> SEQUENCE: 12
 430 Leu Val Pro Arg Gly Ser Ile Glu Gly Arg Gly Gly Arg Ile Phe Tyr
 431 1 5 10 15
 434 Pro Tyr Asp Val Pro Asp Tyr Ala Gly Tyr Pro Tyr Asp Val Pro Asp
 435 20 25 30
 438 Tyr Ala Gly Ser Tyr Pro Tyr Asp Val Pro Asp Tyr Ala Ala Gln Cys
 439 35 40 45
 442 Gly Arg
 443 50
 446 <210> SEQ ID NO: 13
 448 <211> LENGTH: 354
 450 <212> TYPE: DNA
 452 <213> ORGANISM: Aspergillus nidulans

Invalid Response.
 Explain the source of
 genetic material.
 See Item 11 on Error
 Summary sheet.

Same Error

VERIFICATION SUMMARY

DATE: 04/06/2006

PATENT APPLICATION: US/10/572,189

TIME: 10:45:49

Input Set : A:\Sequence Listing (13111-00033-US).txt

Output Set: N:\CRF4\04062006\J572189.raw

L:10 M:270 C: Current Application Number differs, Replaced Current Application No

L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date